

JMS 3/2/01

1652

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/606,129A

DATE: 02/12/2001
 TIME: 15:06:26

Input Set : A:\U607921.app
 Output Set: N:\CRF3\02122001\I606129A.raw

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see page 5

3 <110> APPLICANT: Maines, Mahin D.
 5 <120> TITLE OF INVENTION: BILIVERDIN REDUCTASE FRAGMENTS AND VARIANTS, AND
 6 METHODS OF USING BILIVERDIN REDUCTASE AND SUCH
 7 FRAGMENTS AND VARIANTS
 9 <130> FILE REFERENCE: 176/60792
 11 <140> CURRENT APPLICATION NUMBER: 09/606,129A
 12 <141> CURRENT FILING DATE: 2000-06-28
 14 <150> PRIOR APPLICATION NUMBER: 60/141,309
 15 <151> PRIOR FILING DATE: 1999-06-28
 17 <150> PRIOR APPLICATION NUMBER: 60/163,223
 18 <151> PRIOR FILING DATE: 1999-11-03
 20 <160> NUMBER OF SEQ ID NOS: 37
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 296
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
 30 Met Asn Ala Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
 31 1 5 10 15
 33 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
 34 20 25 30
 36 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
 37 35 40 45
 39 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
 40 50 55 60
 42 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
 43 65 70 75 80
 45 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
 46 85 90 95
 48 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
 49 100 105 110
 51 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
 52 115 120 125
 54 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
 55 130 135 140
 57 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp
 58 145 150 155 160
 60 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
 61 165 170 175
 63 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
 64 180 185 190
 66 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
 67 195 200 205
 69 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
 70 210 215 220
 72 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn

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73 225          230          235          240
75 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
76          245          250          255
78 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
79          260          265          270
81 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
82          275          280          285
84 Gln Lys Tyr Cys Cys Ser Arg Lys
85          290          295
88 <210> SEQ ID NO: 2
89 <211> LENGTH: 1070
90 <212> TYPE: DNA
91 <213> ORGANISM: Homo sapiens
93 <400> SEQUENCE: 2
94 ggggtggcgc ccgagctgc acgagagcgc tgcccytcag tgaccgaaga agagaccaag 60
95 atgaatgcag aqcccgaagc gaagtttggc gtggtggtgg ttggtgttgg ccgagccggc 120
96 tccgtgcgga tgaggggactt gcggaatcca cacccttcct cagcgttcct gaacctgatt 180
97 ggccttcgtt cgagaaggga gctcgggagc attgatggag tccagcagat ttctttggag 240
98 gatgctcttt ccagccaaga ggtggaggtc gccatatctt gcagtggagc ctccagccat 300
99 gaggactaca tcaggcagtt ccttaatgct gccaagcacg tccctgttga ataccocatg 360
100 acactgtcat tggcgccgc tcaggaaactg tgggagctgg ctgagcagaa aggaaaaagtc 420
101 ttgcacgagg agcatgttga actcttgatg gaggaattcg ctctcctgaa aaaagaagtg 480
102 gtggggaaag acctgtgtaa agggctgctc ctcttcacat ctgacccgtt ggaagaagac 540
103 cggtttggct tccctgcatt cagcggcctc tctcgactga cctggctggt cctccctctt 600
104 ggggaagctt ctcttgtgtc tgcactttg gaaqagcgaa aggaagatca gtatatgaaa 660
105 atgacagtgt gtcctggagc agagaagaaa agtccactgt catggattga agaaaaagga 720
106 cctgggtctaa aacgaacag atatttaagc ttccatttca agtctgggtc cttggagaat 780
107 gtgccaaatg taggagttaa taagaacata tttctgaaag atcaaaatat atttgtccag 840
108 aaactcttgg gccagttctc tgagaaggaa ctggctgctg aaaagaaacg catcctgcac 900
109 tgcctggggc ttgcagaaga aatccagaaa tattgctgtt caaggaaagta agaggaggag 960
110 gtgatgtagc acttccaaga tggcaccagc atttggttct tctcaagagt tgaccattat 1020
111 ctctattctt aaaattaaac atgttgggga aacaaaaaaa aaaaaaaaaa 1070
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 296
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 3
120 Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
121 1          5          10          15
123 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
124          20          25          30
126 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
127          35          40          45
129 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
130          50          55          60
132 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
133 65          70          75          80
135 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
136          85          90          95

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138 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
139           100           105           110
141 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
142           115           120           125
144 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
145           130           135           140
147 Leu Leu Lys Gly Ser Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
148 145           150           155           160
150 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
151           165           170           175
153 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
154           180           185           190
156 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
157           195           200           205
159 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
160           210           215           220
162 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
163 225           230           235           240
165 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
166           245           250           255
168 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
169           260           265           270
171 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
172           275           280           285
174 Gln Lys Tyr Cys Cys Ser Arg Lys
175           290           295
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 295
180 <212> TYPE: PRT
181 <213> ORGANISM: Rattus norvegicus
183 <400> SEQUENCE: 4
184 Met Asp Ala Glu Pro Lys Arg Lys Phe Gly Val Val Val Val Gly Val
185 1 5 10 15
187 Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
188 20 25 30
190 Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
191 35 40 45
193 Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
194 50 55 60
196 Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu
197 65 70 75 80
199 Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu
200 85 90 95
202 Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu
203 100 105 110
205 Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu
206 115 120 125
208 Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu
209 130 135 140

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Input Set : A:\U607921.app
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275 <223> OTHER INFORMATION: Description of Artificial Sequence: hydrophobic
276     domain of BVR
278 <220> FEATURE:
279 <221> NAME/KEY: PEPTIDE
280 <222> LOCATION: (2)
281 <223> OTHER INFORMATION: where X is any aa
283 <400> SEQUENCE: 6
W--> 284 Phe Xaa Val Val Val Val
285     1             5
288 <210> SEQ ID NO: 7
289 <211> LENGTH: 6
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
295     binding domain of BVR
297 <220> FEATURE:
298 <221> NAME/KEY: PEPTIDE
299 <222> LOCATION: (2)
300 <223> OTHER INFORMATION: where X is any aa
302 <220> FEATURE:
303 <221> NAME/KEY: PEPTIDE
304 <222> LOCATION: (4)..(5)
305 <223> OTHER INFORMATION: where X is any aa
307 <400> SEQUENCE: 7
W--> 308 Gly Xaa Gly Xaa Xaa Gly
309     1             5
312 <210> SEQ ID NO: 8
313 <211> LENGTH: 8
314 <212> TYPE: PRT
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence:
319     oxidoreductase domain of BVR
321 <400> SEQUENCE: 8
322 Ala Gly Leu His Val Leu Val Glu
323     1             5
326 <210> SEQ ID NO: 9
327 <211> LENGTH: 29
328 <212> TYPE: PRT
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence: leucine
333     zipper of BVR
335 <220> FEATURE:
336 <221> NAME/KEY: PEPTIDE
337 <222> LOCATION: (2)..(7)
338 <223> OTHER INFORMATION: where X is any aa
340 <220> FEATURE:

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\U607921.app
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L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17